

#2

OIPE

RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/935,290

TIME: 17:24:50

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09072001\I935290.raw

3 <110> APPLICANT: Kapeller-Libermann, Rosana
 5 <120> TITLE OF INVENTION: 56919, A NOVEL HUMAN ACYLTRANSFERASE AND USES THEREOF
 7 <130> FILE REFERENCE: MNI-186
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/935,290
 C--> 10 <141> CURRENT FILING DATE: 2001-08-21
 12 <150> PRIOR APPLICATION NUMBER: 60/226,509
 13 <151> PRIOR FILING DATE: 2000-08-21
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3003
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo Sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (341)...(2827)
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (1)...(3003)
 30 <223> OTHER INFORMATION: n = A,T,C or G
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 35 tgtcagcctc tggccgtgca aacaggcacc cagaggaacc agaccttgct tattcaccca 120
 37 cagcctggga ctgtcttctc cagagtctcc atcagctttg ctaatcgact gattggaaat 180
 39 aattcctcaa acaccaccaa gtcaaggata caggcagcag cggtccct gttgtatgga 240
 41 cattctgcac ccgaaactga tagctgagtc ctgaagtttt atgttatgaa acagaagaac 300
 43 ttccatccca gcacatgatt tgggaattac acctgtgac atg gat gaa tct gca 355
 44 Met Asp Glu Ser Ala
 45 1 5
 47 ctg acc ctt ggt aca ata gat gtt tct tat ctg cca cat tca tca gaa 403
 48 Leu Thr Leu Gly Thr Ile Asp Val Ser Tyr Leu Pro His Ser Ser Glu
 49 10 15 20
 51 tac agt gtt ggt cga tgt aag cac aca agt gag gaa tgg ggt gag tgt 451
 52 Tyr Ser Val Gly Arg Cys Lys His Thr Ser Glu Glu Trp Gly Glu Cys
 53 25 30 35
 55 ggc ttt aga ccc acc gtc ttc aga tct gca act tta aaa tgg aaa gaa 499
 56 Gly Phe Arg Pro Thr Val Phe Arg Ser Ala Thr Leu Lys Trp Lys Glu
 57 40 45 50
 59 agc cta atg agt cgg aaa agg cca ttt gtt gga aga tgt tgt tac tcc 547
 60 Ser Leu Met Ser Arg Lys Arg Pro Phe Val Gly Arg Cys Cys Tyr Ser
 61 55 60 65
 63 tgc act ccc cag agc tgg gac aaa ttt ttc aac ccc agt atc ccg tct 595
 64 Cys Thr Pro Gln Ser Trp Asp Lys Phe Phe Asn Pro Ser Ile Pro Ser
 65 70 75 80 85
 67 ttg ggt ttg cgg aat gtt att tat atc aat gaa act cac aca aga cac 643
 68 Leu Gly Leu Arg Asn Val Ile Tyr Ile Asn Glu Thr His Thr Arg His
 69 90 95 100
 71 cgc gga tgg ctt gca aga cgc ctt tct tac gtt ctt ttt att caa gag 691

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72 Arg Gly Trp Leu Ala Arg Arg Leu Ser Tyr Val Leu Phe Ile Gln Glu
73          105          110          115
75 cga gat gtg cat aag ggc atg ttt gcc acc aat gtg act gaa aat gtg 739
76 Arg Asp Val His Lys Gly Met Phe Ala Thr Asn Val Thr Glu Asn Val
77          120          125          130
79 ctg aac agc agt aga gta caa gag gca att gca gaa gtg gct gct gaa 787
80 Leu Asn Ser Ser Arg Val Gln Glu Ala Ile Ala Glu Val Ala Ala Glu
81          135          140          145
83 tta aac cct gat ggt tct gcc cag cag caa tca aaa gcc gtt aac aaa 835
84 Leu Asn Pro Asp Gly Ser Ala Gln Gln Gln Ser Lys Ala Val Asn Lys
85 150          155          160          165
87 gtg aaa aag aaa gct aaa agg att ctt caa gaa atg gtt gcc act gtc 883
88 Val Lys Lys Lys Ala Lys Arg Ile Leu Gln Glu Met Val Ala Thr Val
89          170          175          180
91 tca ccg gca atg atc aga ctg act ggg tgg gtg ctg cta aaa ctg ttc 931
92 Ser Pro Ala Met Ile Arg Leu Thr Gly Trp Val Leu Leu Lys Leu Phe
93          185          190          195
95 aac agc ttc ttt tgg aac att caa att cac aaa ggt caa ctt gag atg 979
96 Asn Ser Phe Phe Trp Asn Ile Gln Ile His Lys Gly Gln Leu Glu Met
97          200          205          210
99 gtt aaa gct gca act gag acg aat ttg ccg ctt ctg ttt cta cca gtt 1027
100 Val Lys Ala Ala Thr Glu Thr Asn Leu Pro Leu Leu Phe Leu Pro Val
101          215          220          225
103 cat aga tcc cat att gac tat ctg ctg ctc act ttc att ctc ttc tgc 1075
104 His Arg Ser His Ile Asp Tyr Leu Leu Leu Thr Phe Ile Leu Phe Cys
105 230          235          240          245
107 cat aac atc aaa gca cca tac att gct tca ggc aat aat ctc aac atc 1123
108 His Asn Ile Lys Ala Pro Tyr Ile Ala Ser Gly Asn Asn Leu Asn Ile
109          250          255          260
111 cca atc ttc agt acc ttg atc cat aag ctt ggg ggc ttc ttc ata cga 1171
112 Pro Ile Phe Ser Thr Leu Ile His Lys Leu Gly Gly Phe Phe Ile Arg
113          265          270          275
115 cga agg ctc gat gaa aca cca gat gga cgg aaa gat gtt ctc tat aga 1219
116 Arg Arg Leu Asp Glu Thr Pro Asp Gly Arg Lys Asp Val Leu Tyr Arg
117          280          285          290
119 gct ttg ctc cat ggg cat ata gtt gaa tta ctt cga cag cag caa ttc 1267
120 Ala Leu Leu His Gly His Ile Val Glu Leu Leu Arg Gln Gln Gln Phe
121          295          300          305
123 ttg gag atc ttc ctg gaa ggc aca cgt tct agg agt gga aaa acc tct 1315
124 Leu Glu Ile Phe Leu Glu Gly Thr Arg Ser Arg Ser Gly Lys Thr Ser
125 310          315          320          325
127 tgt gct cgg gca gga ctt ttg tca gtt gtg gta gat act ctg tct acc 1363
128 Cys Ala Arg Ala Gly Leu Leu Ser Val Val Val Asp Thr Leu Ser Thr
129          330          335          340
131 aat gtc atc cca gac atc ttg ata ata cct gtt gga atc tcc tat gat 1411
132 Asn Val Ile Pro Asp Ile Leu Ile Ile Pro Val Gly Ile Ser Tyr Asp
133          345          350          355
135 cgc att atc gaa ggt cac tac aat ggt gaa caa ctg ggc aaa cct aag 1459
136 Arg Ile Ile Glu Gly His Tyr Asn Gly Glu Gln Leu Gly Lys Pro Lys

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137	360	365	370	
139	aag aat gag agc ctg tgg agt gta gca aga ggt gtt att aga atg tta	1507		
140	Lys Asn Glu Ser Leu Trp Ser Val Ala Arg Gly Val Ile Arg Met Leu			
141	375	380	385	
143	cga aaa aac tat ggt tgt gtc cga gtg gat ttt gca cag cca ttt tcc	1555		
144	Arg Lys Asn Tyr Gly Cys Val Arg Val Asp Phe Ala Gln Pro Phe Ser			
145	390	395	400	405
147	tta aag gaa tat tta gaa agc caa agt cag aaa ccg gtg tct gct cta	1603		
148	Leu Lys Glu Tyr Leu Glu Ser Gln Ser Gln Lys Pro Val Ser Ala Leu			
149	410	415	420	
151	ctt tcc ctg gag caa gcg ttg tta cca gct ata ctt cct tca aga ccc	1651		
152	Leu Ser Leu Glu Gln Ala Leu Leu Pro Ala Ile Leu Pro Ser Arg Pro			
153	425	430	435	
155	agt gat gct gct gat gaa ggt aga gac acg tcc att aat gag tcc aga	1699		
156	Ser Asp Ala Ala Asp Glu Gly Arg Asp Thr Ser Ile Asn Glu Ser Arg			
157	440	445	450	
159	aat gca aca gat gaa tcc cta cga agg agg ttg att gca aat ctg gct	1747		
160	Asn Ala Thr Asp Glu Ser Leu Arg Arg Arg Leu Ile Ala Asn Leu Ala			
161	455	460	465	
163	gag cat att cta ttc act gct agc aag tcc tgt gcc att atg tcc aca	1795		
164	Glu His Ile Leu Phe Thr Ala Ser Lys Ser Cys Ala Ile Met Ser Thr			
165	470	475	480	485
167	cac att gtg gct tgc ctg ctc ctc tac aga cac agg cag gga att gat	1843		
168	His Ile Val Ala Cys Leu Leu Leu Tyr Arg His Arg Gln Gly Ile Asp			
169	490	495	500	
171	ctc tcc aca ttg gtc gaa gac ttc ttt gtg atg aaa gag gaa gtc ctg	1891		
172	Leu Ser Thr Leu Val Glu Asp Phe Phe Val Met Lys Glu Glu Val Leu			
173	505	510	515	
175	gct cgt gat ttt gac ctg ggg ttc tca gga aat tca gaa gat gta gta	1939		
176	Ala Arg Asp Phe Asp Leu Gly Phe Ser Gly Asn Ser Glu Asp Val Val			
177	520	525	530	
179	atg cat gcc ata cag ctg ctg gga aat tgt gtc aca atc acc cac act	1987		
180	Met His Ala Ile Gln Leu Leu Gly Asn Cys Val Thr Ile Thr His Thr			
181	535	540	545	
183	agc agg aac gat gag ttt ttt atc acc ccc agc aca act gtc cca tca	2035		
184	Ser Arg Asn Asp Glu Phe Phe Ile Thr Pro Ser Thr Thr Val Pro Ser			
185	550	555	560	565
187	gtc ttc gaa ctc aac ttc tac agc aat ggg gta ctt cat gtc ttt atc	2083		
188	Val Phe Glu Leu Asn Phe Tyr Ser Asn Gly Val Leu His Val Phe Ile			
189	570	575	580	
191	atg gag gcc atc ata gct tgc agc ctt tat gca gtt ctg aac aag agg	2131		
192	Met Glu Ala Ile Ala Cys Ser Leu Tyr Ala Val Leu Asn Lys Arg			
193	585	590	595	
195	gga ctg ggg ggt ccc act agc acc cca cct aac ctg atc agc cag gag	2179		
196	Gly Leu Gly Gly Pro Thr Ser Thr Pro Pro Asn Leu Ile Ser Gln Glu			
197	600	605	610	
199	cag ctg gtg cgg aag gcg gcc agc ctg tgc tac ctt ctc tcc aat gaa	2227		
200	Gln Leu Val Arg Lys Ala Ala Ser Leu Cys Tyr Leu Leu Ser Asn Glu			
201	615	620	625	

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203 ggc acc atc tca ctg cct tgc cag aca ttt tac caa gtc tgc cat gaa 2275
204 Gly Thr Ile Ser Leu Pro Cys Gln Thr Phe Tyr Gln Val Cys His Glu
205 630 635 640 645
207 aca gta gga aag ttt atc cag tat ggc att ctt aca gtg gca gag cac 2323
208 Thr Val Gly Lys Phe Ile Gln Tyr Gly Ile Leu Thr Val Ala Glu His
209 650 655 660
211 gat gac cag gaa gat atc agt cct agt ctt gct gag cag cag tgg gac 2371
212 Asp Asp Gln Glu Asp Ile Ser Pro Ser Leu Ala Glu Gln Gln Trp Asp
213 665 670 675
215 aag aag ctt cca gaa cct ttg tct tgg aga agt gat gaa gaa gat gaa 2419
216 Lys Lys Leu Pro Glu Pro Leu Ser Trp Arg Ser Asp Glu Glu Asp Glu
217 680 685 690
219 gac agt gac ttt ggg gag gaa cag cga gat tgc tac ctg aag gtg agc 2467
220 Asp Ser Asp Phe Gly Glu Glu Gln Arg Asp Cys Tyr Leu Lys Val Ser
221 695 700 705
223 caa tcc aag gag cac cag cag ttt atc acc ttc tta cag aga ctc ctt 2515
224 Gln Ser Lys Glu His Gln Gln Phe Ile Thr Phe Leu Gln Arg Leu Leu
225 710 715 720 725
227 ggg cct ttg ctg gag gcc tac agc tct gct gcc atc ttt gtt cac aac 2563
228 Gly Pro Leu Leu Glu Ala Tyr Ser Ser Ala Ala Ile Phe Val His Asn
229 730 735 740
231 ttc agt ggt cct gtt cca gaa cct gag tat ctg caa aag ttg cac aaa 2611
232 Phe Ser Gly Pro Val Pro Glu Pro Glu Tyr Leu Gln Lys Leu His Lys
233 745 750 755
235 tac cta ata acc aga aca gaa aga aat gtt gca gta tat gct gag agt 2659
236 Tyr Leu Ile Thr Arg Thr Glu Arg Asn Val Ala Val Tyr Ala Glu Ser
237 760 765 770
239 gcc aca tat tgt ctt gtg aag aat gct gtg aaa atg ttt aag gat att 2707
240 Ala Thr Tyr Cys Leu Val Lys Asn Ala Val Lys Met Phe Lys Asp Ile
241 775 780 785
243 ggg gtt ttc aag gag acc aaa caa aag aga gtg tct gtt tta gaa ctg 2755
244 Gly Val Phe Lys Glu Thr Lys Gln Lys Arg Val Ser Val Leu Glu Leu
245 790 795 800 805
247 agc agc act ttt cta cct caa tgc aac cga caa aaa ctt cta gaa tat 2803
248 Ser Ser Thr Phe Leu Pro Gln Cys Asn Arg Gln Lys Leu Leu Glu Tyr
249 810 815 820
251 att ctg agt ttt gtg gtg ctg tag gtaacgtgtg gcaactgctgg caaatgaagg 2857
252 Ile Leu Ser Phe Val Val Leu
253 825
255 tcatgagatg agttccttgt aggtaccagc ttctggctca agagtttgaa ggtgccttcg 2917
W--> 257 caggggtcag gcttgccttg tncccaagtg atctcctgga agacaagtgc cttctnccctc 2977 OK
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262 <210> SEQ ID NO: 2
263 <211> LENGTH: 828
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 2
268 Met Asp Glu Ser Ala Leu Thr Leu Gly Thr Ile Asp Val Ser Tyr Leu
269 1 5 10 15

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271 Pro His Ser Ser Glu Tyr Ser Val Gly Arg Cys Lys His Thr Ser Glu
272          20          25          30
274 Glu Trp Gly Glu Cys Gly Phe Arg Pro Thr Val Phe Arg Ser Ala Thr
275          35          40          45
277 Leu Lys Trp Lys Glu Ser Leu Met Ser Arg Lys Arg Pro Phe Val Gly
278          50          55          60
280 Arg Cys Cys Tyr Ser Cys Thr Pro Gln Ser Trp Asp Lys Phe Phe Asn
281 65          70          75          80
283 Pro Ser Ile Pro Ser Leu Gly Leu Arg Asn Val Ile Tyr Ile Asn Glu
284          85          90          95
286 Thr His Thr Arg His Arg Gly Trp Leu Ala Arg Arg Leu Ser Tyr Val
287          100         105         110
289 Leu Phe Ile Gln Glu Arg Asp Val His Lys Gly Met Phe Ala Thr Asn
290          115         120         125
292 Val Thr Glu Asn Val Leu Asn Ser Ser Arg Val Gln Glu Ala Ile Ala
293          130         135         140
295 Glu Val Ala Ala Glu Leu Asn Pro Asp Gly Ser Ala Gln Gln Gln Ser
296 145          150         155         160
298 Lys Ala Val Asn Lys Val Lys Lys Lys Ala Lys Arg Ile Leu Gln Glu
299          165         170         175
301 Met Val Ala Thr Val Ser Pro Ala Met Ile Arg Leu Thr Gly Trp Val
302          180         185         190
304 Leu Leu Lys Leu Phe Asn Ser Phe Phe Trp Asn Ile Gln Ile His Lys
305          195         200         205
307 Gly Gln Leu Glu Met Val Lys Ala Ala Thr Glu Thr Asn Leu Pro Leu
308          210         215         220
310 Leu Phe Leu Pro Val His Arg Ser His Ile Asp Tyr Leu Leu Leu Thr
311 225          230         235         240
313 Phe Ile Leu Phe Cys His Asn Ile Lys Ala Pro Tyr Ile Ala Ser Gly
314          245         250         255
316 Asn Asn Leu Asn Ile Pro Ile Phe Ser Thr Leu Ile His Lys Leu Gly
317          260         265         270
319 Gly Phe Phe Ile Arg Arg Arg Leu Asp Glu Thr Pro Asp Gly Arg Lys
320          275         280         285
322 Asp Val Leu Tyr Arg Ala Leu Leu His Gly His Ile Val Glu Leu Leu
323          290         295         300
325 Arg Gln Gln Gln Phe Leu Glu Ile Phe Leu Glu Gly Thr Arg Ser Arg
326 305          310         315         320
328 Ser Gly Lys Thr Ser Cys Ala Arg Ala Gly Leu Leu Ser Val Val Val
329          325         330         335
331 Asp Thr Leu Ser Thr Asn Val Ile Pro Asp Ile Leu Ile Ile Pro Val
332          340         345         350
334 Gly Ile Ser Tyr Asp Arg Ile Ile Glu Gly His Tyr Asn Gly Glu Gln
335          355         360         365
337 Leu Gly Lys Pro Lys Lys Asn Glu Ser Leu Trp Ser Val Ala Arg Gly
338          370         375         380
340 Val Ile Arg Met Leu Arg Lys Asn Tyr Gly Cys Val Arg Val Asp Phe
341 385          390         395         400
343 Ala Gln Pro Phe Ser Leu Lys Glu Tyr Leu Glu Ser Gln Ser Gln Lys

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VERIFICATION SUMMARY

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DATE: 09/07/2001

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Input Set : A:\Seqlist.txt

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1